PAGE: 1   **RAW SEQUENCE LISTING**
PATENT APPLICATION *US/08/699,716*   DATE: 11/13/96
TIME: 14:49:38

INPUT SET: S13766.raw

> **This Raw Listing contains the General Information Section and up to the first 5 pages.**

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4   (i) APPLICANT: David G. Heath
 5   Arthur M. Friedlander
 6   George W. Anderson
 7   Susan L. Welkos
 8
 9   (ii) TITLE OF INVENTION: Recombinant F1-V Plague Vaccine
10
11   (iii) NUMBER OF SEQUENCES:   6
12
13   (iv) CORRESPONDENCE ADDRESS:
14   (A) ADDRESSEE:   John Moran
15   (B) STREET:   USA MRMC -  MRMC-JA
16   (C) CITY: FORT DETRICK, FREDERICK
17   (D) STATE: MARYLAND
18   (E) COUNTRY: USA
19   (F) ZIP: 21702-5012
20
21   (v) COMPUTER READABLE FORM:
22   (A) MEDIUM TYPE: Floppy disk
23   (B) COMPUTER: Apple Macintosh
24   (C) OPERATING SYSTEM: Macintosh 7.5
25   (D) SOFTWARE: Microsoft Word 6.0
26
27   (vi) CURRENT APPLICATION DATA:
28   (A) APPLICATION NUMBER:
29   (B) FILING DATE:
30   (C) CLASSIFICATION:
31
32   (vii) PRIOR APPLICATION DATA:
33   (A) APPLICATION NUMBER:
34   (B) FILING DATE:
35
36   (viii) ATTORNEY/AGENT INFORMATION:
37   (A) NAME: Moran, John
38   (B) REGISTRATION NUMBER: 26,313
39   (C) REFERENCE/DOCKET NUMBER:
40
41   (ix) TELECOMMUNICATION INFORMATION
42   (A) TELEPHONE: (301) 619-2065
43   (B) TELEFAX:  (301) 619-7714
44
45   (2) INFORMATION FOR SEQ ID NO:1:
46
```

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/699,716*

DATE: 11/13/96
TIME: 14:49:41

INPUT SET: S13766.raw

```
47    (i) SEQUENCE CHARACTERISTICS:
48    (A) LENGTH: 1566 bp
49    (B) TYPE: Nucleic acid
50    (C) STRANDEDNESS: Single
51    (D) TOPOLOGY: Linear
52
53    (ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:
54
55    ATGGGCCATC  ATCATCATCA  TCATCATCAT  CATCACAGCA       40
56
57    GCGGCCATAT  CGACGACGAC  GACAAGCATA  TGAAAAAAAT       80
58
59    CAGTTCCGTT  ATCGCCATTG  CATTATTTGG  AACTATTGCA      120
60
61    ACTGCTAATG  CGGCAGATTT  AACTGCAAGC  ACCACTGCAA      160
62
63    CGGCAACTCT  TGTTGAACCA  GCCCGCATCA  CTCTTACATA      200
64
65    TAAGGAAGGC  GCTCCAATTA  CAATTATGGA  CAATGGAAAC      240
66
67    ATCGATACAG  AATTACTTGT  TGGTACGCTT  ACTCTTGGCG      280
68
69    GCTATAAAAC  AGGAACCACT  AGCACATCTG  TTAACTTTAC      320
70
71    AGATGCCGCG  GGTGATCCCA  TGTACTTAAC  ATTTACTTCT      360
72
73    CAGGATGGAA  ATAACCACCA  ATTCACTACA  AAAGTGATTG      400
74
75    GCAAGGATTC  TAGAGATTTT  GATATCTCTC  CTAAGGTAAA      440
76
77    CGGTGAGAAC  CTTGTGGGGG  ATGACGTCGT  CTTGGCTACG      480
78
79    GGCAGCCAGG  ATTTCTTTGT  TCGCTCAATT  GGTTCCAAAG      520
80
81    GCGGTAAACT  TGCAGCAGGT  AAATACACTG  ATGCTGTAAC      560
82
83    CGTAACCGTA  TCTAACCAAG  AATTCATGAT  TAGAGCCTAC      600
84
85    GAACAAAACC  CACAACATTT  TATTGAGGAT  CTAGAAAAAG      640
86
87    TTAGGGTGGA  ACAACTTACT  GGTCATGGTT  CTTCAGTTTT      680
88
89    AGAAGAATTG  GTTCAGTTAG  TCAAAGATAA  AAATATAGAT      720
90
91    ATTTCCATTA  AATATGATCC  CAGAAAAGAT  TCGGAGGTTT      760
92
93    TTGCCAATAG  AGTAATTACT  GATGATATCG  AATTGCTCAA      800
94
95    GAAAATCCTA  GCTTATTTTC  TACCCGAGGA  TACCATTCTT      840
96
97    AAAGGCGGTC  ATTATGACAA  CCAACTGCAA  AATGGCATCA      880
98
99    AGCGAGTAAA  AGAGTTCCTT  GAATCATCGC  CGAATACACA      920
```

INPUT SET: S13766.raw

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100
101   ATGGGAATTG   CGGGCGTTCA   TGGCAGTAAT   GCATTTCTCT        960
102
103   TTAACCGCCG   ATCGTATCGA   TGATGATATT   TTGAAAGTGA       1000
104
105   TTGTTGATTC   AATGAATCAT   CATGGTGATG   CCCGTAGCAA       1040
106
107   GTTGCGTGAA   GAATTAGCTG   AGCTTACCGC   CGAATTAAAG       1080
108
109   ATTTATTCAG   TTATTCAAGC   CGAAATTAAT   AAGCATCTGT       1120
110
111   CTAGTAGTGG   CACCATAAAT   ATCCATGATA   AATCCATTAA       1160
112
113   TCTCATGGAT   AAAAATTTAT   ATGGTTATAC   AGATGAAGAG       1200
114
115   ATTTTTAAAG   CCAGCGCAGA   GTACAAAATT   CTCGAGAAAA       1240
116
117   TGCCTCAAAC   CACCATTCAG   GTGGATGGGA   GCGAGAAAAA       1280
118
119   AATAGTCTCG   ATAAAGGACT   TTCTTGGAAG   TGAGAATAAA       1320
120
121   AGAACCGGGG   CGTTGGGTAA   TCTGAAAAAC   TCATACTCTT       1360
122
123   ATAATAAAGA   TAATAATGAA   TTATCTCACT   TTGCCACCAC       1400
124
125   CTGCTCGGAT   AAGTCCAGGC   CGCTCAACGA   CTTGGTTAGC       1440
126
127   CAAAAAACAA   CTCAGCTGTC   TGATATTACA   TCACGTTTTA       1480
128
129   ATTCAGCTAT   TGAAGCACTG   AACCGTTTCA   TTCAGAAATA       1520
130
131   TGATTCAGTG   ATGCAACGTC   TGCTAGATGA   CACGTCTGGT       1560
132
133   AAATGA                                                  1566
134
135
136   (2)  INFORMATION FOR SEQ ID NO:2:
137
138   (i)  SEQUENCE CHARACTERISTICS:
139   (A)  LENGTH: 521
140   (B)  TYPE:Amino acid
141   (C)  STRANDEDNESS: Single
142   (D)  TOPOLOGY: Linear
143
144   (ii) SEQUENCE DESCRIPTION: SEQ ID NO:2:
145
146   Met Gly His His His His His His His His His Ser Ser Gly
147   1               5                   10                  15
148
149   His Ile Asp Asp Asp Asp Lys His Met Lys Lys Ile Ser Ser Val
150                   20                  25                  30
151
152   Ile Ala Ile Ala Leu Phe Gly Thr Ile Ala Thr Ala Asn Ala Ala
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153                     35                    40                    45
154
155    Asp Leu Thr Ala Ser Thr Thr Ala Thr Ala Thr Leu Val Glu Pro
156                     50                    55                    60
157
158    Ala Arg Ile Thr Leu Thr Tyr Lys Glu Gly Ala Pro Ile Thr Ile
159                     65                    70                    75
160
161    Met Asp Asn Gly Asn Ile Asp Thr Glu Leu Leu Val Gly Thr Leu
162                     80                    85                    90
163
164    Thr Leu Gly Gly Tyr Lys Thr Gly Thr Thr Ser Thr Ser Val Asn
165                     95                    100                   105
166
167    Phe Thr Asp Ala Ala Gly Asp Pro Met Tyr Leu Thr Phe Thr Ser
168                     110                   115                   120
169
170    Gln Asp Gly Asn Asn His Gln Phe Thr Thr Lys Val Ile Gly Lys
171                     125                   130                   135
172
173    Asp Ser Arg Asp Phe Asp Ile Ser Pro Lys Val Asn Gly Glu Asn
174                     140                   145                   150
175
176    Leu Val Gly Asp Asp Val Val Leu Ala Thr Gly Ser Gln Asp Phe
177                     155                   160                   165
178
179    Phe Val Arg Ser Ile Gly Ser Lys Gly Gly Lys Leu Ala Ala Gly
180                     170                   175                   180
181
182    Lys Tyr Thr Asp Ala Val Thr Val Thr Val Ser Asn Gln Glu Phe
183                     185                   190                   195
184
185    Met Ile Arg Ala Tyr Glu Gln Asn Pro Gln His Phe Ile Glu Asp
186                     200                   205                   210
187
188    Leu Glu Lys Val Arg Val Glu Gln Leu Thr Gly His Gly Ser Ser
189                     215                   220                   225
190
191    Val Leu Glu Glu Leu Val Gln Leu Val Lys Asp Lys Asn Ile Asp
192                     230                   235                   240
193
194    Ile Ser Ile Lys Tyr Asp Pro Arg Lys Asp Ser Glu Val Phe Ala
195                     245                   250                   255
196
197    Asn Arg Val Ile Thr Asp Asp Ile Glu Leu Leu Lys Lys Ile Leu
198                     260                   265                   270
199
200    Ala Tyr Phe Leu Pro Glu Asp Thr Ile Leu Lys Gly Gly His Tyr
201                     275                   280                   285
202
203    Asp Asn Gln Leu Gln Asn Gly Ile Lys Arg Val Lys Glu Phe Leu
204                     290                   295                   300
205
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206    Glu Ser Ser Pro Asn Thr Gln Trp Glu Leu Arg Ala Phe Met Ala
207                    305             310             315

208
209    Val Met His Phe Ser Leu Thr Ala Asp Arg Ile Asp Asp Asp Ile
210                    320             325             330

211
212    Leu Lys Val Ile Val Asp Ser Met Asn His His Gly Asp Ala Arg
213                    335             340             345

214
215    Ser Lys Leu Arg Glu Glu Leu Ala Glu Leu Thr Ala Glu Leu Lys
216                    350             355             360

217
218    Ile Tyr Ser Val Ile Gln Ala Glu Ile Asn Lys His Leu Ser Ser
219                    365             370             375

220
221    Ser Gly Thr Ile Asn Ile His Asp Lys Ser Ile Asn Leu Met Asp
222                    380             385             390

223
224    Lys Asn Leu Tyr Gly Tyr Thr Asp Glu Glu Ile Phe Lys Ala Ser
225                    395             400             405

226
227    Ala Glu Tyr Lys Ile Leu Glu Lys Met Pro Gln Thr Thr Ile Gln
228                    410             415             420

229
230    Val Asp Gly Ser Glu Lys Lys Ile Val Ser Ile Lys Asp Phe Leu
231                    425             430             435

232
233    Gly Ser Glu Asn Lys Arg Thr Gly Ala Leu Gly Asn Leu Lys Asn
234                    440             445             450

235
236    Ser Tyr Ser Tyr Asn Lys Asp Asn Asn Glu Leu Ser His Phe Ala
237                    455             460             465

238
239    Thr Thr Cys Ser Asp Lys Ser Arg Pro Leu Asn Asp Leu Val Ser
240                    470             475             480

241
242    Gln Lys Thr Thr Gln Leu Ser Asp Ile Thr Ser Arg Phe Asn Ser
243                    485             490             495

244
245    Ala Ile Glu Ala Leu Asn Arg Phe Ile Gln Lys Tyr Asp Ser Val
246                    500             505             510

247
248    Met Gln Arg Leu Leu Asp Asp Thr Ser Gly Lys
249                    515             520

250
251
252    (2) INFORMATION FOR SEQ ID NO:3:
253
254    (i) SEQUENCE CHARACTERISTICS:
255    (A) LENGTH: 28 bp
256    (B) TYPE: Nucleic acid
257    (C) STRANDEDNESS: Single
258    (D) TOPOLOGY: Linear
```